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## RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/10/040,863

TIME: 08:51:13

Input Set : N:\Crf3\RULE60\10040863.raw

Output Set: N:\CRF3\02112002\J040863.raw

1 <110> APPLICANT: Eric H. Holmes et al.  
 2 <120> TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE  
 3 GM1-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES  
 4 THEREOF  
 5 <130> FILE REFERENCE: 8511-029  
 6 <140> CURRENT APPLICATION NUMBER: US/10/040,863  
 7 <141> CURRENT FILING DATE: 2001-11-01  
 8 <150> PRIOR APPLICATION NUMBER: US/09/298,886  
 9 <151> PRIOR FILING DATE: 1999-04-23  
 10 <160> NUMBER OF SEQ ID NOS: 29  
 11 <170> SOFTWARE: PatentIn Ver. 2.0  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 22  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Artificial Sequence  
 17 <220> FEATURE:  
 18 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 19 <400> SEQUENCE: 1  
 20 ggccgctttg ggaaccagat gg 22  
 22 <210> SEQ ID NO: 2  
 23 <211> LENGTH: 22  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Artificial Sequence  
 26 <220> FEATURE:  
 27 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 28 <400> SEQUENCE: 2  
 29 ggttacactg cgtgagcagc gc 22  
 31 <210> SEQ ID NO: 3  
 32 <211> LENGTH: 24  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Artificial Sequence  
 35 <220> FEATURE:  
 36 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 37 <400> SEQUENCE: 3  
 38 ttcccatcag aaggctcttc ctgc 24  
 40 <210> SEQ ID NO: 4  
 41 <211> LENGTH: 17  
 42 <212> TYPE: DNA  
 43 <213> ORGANISM: Artificial Sequence  
 44 <220> FEATURE:  
 45 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 46 <400> SEQUENCE: 4  
 47 ccgcctccac catcttc 17

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49 <210> SEQ ID NO: 5
50 <211> LENGTH: 24
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
55 <400> SEQUENCE: 5
56   atgaattccc tccagcagcg aata                                24
58 <210> SEQ ID NO: 6
59 <211> LENGTH: 24
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
64 <400> SEQUENCE: 6
65   gccatggcca gcgcccaggt tcct                                24
67 <210> SEQ ID NO: 7
68 <211> LENGTH: 1149
69 <212> TYPE: DNA
70 <213> ORGANISM: Rattus norvegicus
71 <220> FEATURE:
72 <221> NAME/KEY: CDS
73 <222> LOCATION: (1)..(1143)
74 <400> SEQUENCE: 7
75   atg gcc agc gcc cag gtt cct ttc tcc ttt cct ctg gcc cac ttc ctc  48
76   Met Ala Ser Ala Gln Val Pro Phe Ser Phe Pro Leu Ala His Phe Leu
77   1          5          10          15
78   atc ttt gtc ttc gtg act tcc acc atc atc cac ctc cag cag cga ata  96
79   Ile Phe Val Phe Val Thr Ser Thr Ile His Leu Gln Gln Arg Ile
80   20          25          30
81   gtg aag ctc caa ccc ctg tca gag aag gaa tta ccg atg acg act caa  144
82   Val Lys Leu Gln Pro Leu Ser Glu Lys Glu Leu Pro Met Thr Thr Gln
83   35          40          45
84   atg tcc tcg gga aac aca gaa agc cca gag atg cga cgg gac agc gag  192
85   Met Ser Ser Gly Asn Thr Glu Ser Pro Glu Met Arg Arg Asp Ser Glu
86   50          55          60
87   cag cat ggg aat gga gag ctg cgg ggc atg ttc acg atc aat tcc att  240
88   Gln His Gly Asn Gly Glu Leu Arg Gly Met Phe Thr Ile Asn Ser Ile
89   65          70          75          80
90   ggc cgg ctg ggg aac cag atg ggc gaa tac gcc aca ctc ttt gca ctg  288
91   Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr Leu Phe Ala Leu
92   85          90          95
93   gcc agg atg aac gga cgg ctt gcg ttc atc ccc gca tcc atg cac aac  336
94   Ala Arg Met Asn Gly Arg Leu Ala Phe Ile Pro Ala Ser Met His Asn
95   100         105         110
96   gct cta gcg ccc atc ttc agg atc agc ctc ccg gtg tta cac agc gac  384
97   Ala Leu Ala Pro Ile Phe Arg Ile Ser Leu Pro Val Leu His Ser Asp
98   115        120        125
99   acg gcc aaa aag atc cca tgg cag aat tac cat ctc aac gac tgg atg  432

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100  Thr Ala Lys Lys Ile Pro Trp Gln Asn Tyr His Leu Asn Asp Trp Met
101      130                      135                      140
102  gag gag cgt tac cgc cac att ccg gga cac ttt gtg cgc ttc acg gga 480
103  Glu Glu Arg Tyr Arg His Ile Pro Gly His Phe Val Arg Phe Thr Gly
104      145                      150                      155                      160
105  tac ccg tgc tcc tgg acc ttc tac cac cac ctg cgc cca gag atc ctg 528
106  Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu Arg Pro Glu Ile Leu
107                      165                      170                      175
108  aag gag ttc acc ctg cat gac cac gtg cgg gag gag gcc cag gcc ttc 576
109  Lys Glu Phe Thr Leu His Asp His Val Arg Glu Glu Ala Gln Ala Phe
110                      180                      185                      190
111  ctg cgt ggt ctg cgg gtg aat ggg agc cag ccg agt act ttt gtg ggt 624
112  Leu Arg Gly Leu Arg Val Asn Gly Ser Gln Pro Ser Thr Phe Val Gly
113      195                      200                      205
114  gtc cat gtg cgc cga ggg gac tat gtg cat gtc atg cct aat gtg tgg 672
115  Val His Val Arg Arg Gly Asp Tyr Val His Val Met Pro Asn Val Trp
116      210                      215                      220
117  aag ggc gtg gtg gct gac cgg ggt tac ctg gaa aag gcc ctg gat atg 720
118  Lys Gly Val Val Ala Asp Arg Gly Tyr Leu Glu Lys Ala Leu Asp Met
119      225                      230                      235                      240
120  ttc cgg gca cgc tat tca tct cca gtc ttc gtg gtt aca agc aac ggt 768
121  Phe Arg Ala Arg Tyr Ser Ser Pro Val Phe Val Val Thr Ser Asn Gly
122                      245                      250                      255
123  atg gcc tgg tgc cgg gag aac att aat gct tcc cga gga gac gtg gtg 816
124  Met Ala Trp Cys Arg Glu Asn Ile Asn Ala Ser Arg Gly Asp Val Val
125      260                      265                      270
126  ttc gcg ggc aat ggt att gag ggg tcg cca gcc aag gac ttc gcg ctg 864
127  Phe Ala Gly Asn Gly Ile Glu Gly Ser Pro Ala Lys Asp Phe Ala Leu
128      275                      280                      285
129  ctc acc cag tgc aac cac acc atc atg act att ggg acc ttt ggg att 912
130  Leu Thr Gln Cys Asn His Thr Ile Met Thr Ile Gly Thr Phe Gly Ile
131      290                      295                      300
132  tgg gct gcc tac ctg gca ggt ggt gat acc atc tac tta gcc aac tac 960
133  Trp Ala Ala Tyr Leu Ala Gly Gly Asp Thr Ile Tyr Leu Ala Asn Tyr
134      305                      310                      315                      320
135  acc ctt ccg gat tct ccg ttc ctc aaa gtc ttt aag cca gag gca gcc 1008
136  Thr Leu Pro Asp Ser Pro Phe Leu Lys Val Phe Lys Pro Glu Ala Ala
137                      325                      330                      335
138  ttc cta ccc gaa tgg gtg ggc atc cct gcc gat ctg tcc cca ctc ctt 1056
139  Phe Leu Pro Glu Trp Val Gly Ile Pro Ala Asp Leu Ser Pro Leu Leu
140      340                      345                      350
141  aag gca tta aca cca gcc tgt cct cgg tcc cac ttc cac ctc aag gca 1104
142  Lys Ala Leu Thr Pro Ala Cys Pro Arg Ser His Phe His Leu Lys Ala
143      355                      360                      365
144  aaa gga gtc act tgt tac gtc gca gga aga gcc ttc tga tgggaa 1149
145  Lys Gly Val Thr Cys Tyr Val Ala Gly Arg Ala Phe
146      370                      375                      380
148 <210> SEQ ID NO: 8
149 <211> LENGTH: 380

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150 <212> TYPE: PRT
151 <213> ORGANISM: Rattus norvegicus
152 <400> SEQUENCE: 8
153 Met Ala Ser Ala Gln Val Pro Phe Ser Phe Pro Leu Ala His Phe Leu
154 1 5 10 15
155 Ile Phe Val Phe Val Thr Ser Thr Ile Ile His Leu Gln Gln Arg Ile
156 20 25 30
157 Val Lys Leu Gln Pro Leu Ser Glu Lys Glu Leu Pro Met Thr Thr Gln
158 35 40 45
159 Met Ser Ser Gly Asn Thr Glu Ser Pro Glu Met Arg Arg Asp Ser Glu
160 50 55 60
161 Gln His Gly Asn Gly Glu Leu Arg Gly Met Phe Thr Ile Asn Ser Ile
162 65 70 75 80
163 Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr Leu Phe Ala Leu
164 85 90 95
165 Ala Arg Met Asn Gly Arg Leu Ala Phe Ile Pro Ala Ser Met His Asn
166 100 105 110
167 Ala Leu Ala Pro Ile Phe Arg Ile Ser Leu Pro Val Leu His Ser Asp
168 115 120 125
169 Thr Ala Lys Lys Ile Pro Trp Gln Asn Tyr His Leu Asn Asp Trp Met
170 130 135 140
171 Glu Glu Arg Tyr Arg His Ile Pro Gly His Phe Val Arg Phe Thr Gly
172 145 150 155 160
173 Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu Arg Pro Glu Ile Leu
174 165 170 175
175 Lys Glu Phe Thr Leu His Asp His Val Arg Glu Glu Ala Gln Ala Phe
176 180 185 190
177 Leu Arg Gly Leu Arg Val Asn Gly Ser Gln Pro Ser Thr Phe Val Gly
178 195 200 205
179 Val His Val Arg Arg Gly Asp Tyr Val His Val Met Pro Asn Val Trp
180 210 215 220
181 Lys Gly Val Val Ala Asp Arg Gly Tyr Leu Glu Lys Ala Leu Asp Met
182 225 230 235 240
183 Phe Arg Ala Arg Tyr Ser Ser Pro Val Phe Val Val Thr Ser Asn Gly
184 245 250 255
185 Met Ala Trp Cys Arg Glu Asn Ile Asn Ala Ser Arg Gly Asp Val Val
186 260 265 270
187 Phe Ala Gly Asn Gly Ile Glu Gly Ser Pro Ala Lys Asp Phe Ala Leu
188 275 280 285
189 Leu Thr Gln Cys Asn His Thr Ile Met Thr Ile Gly Thr Phe Gly Ile
190 290 295 300
191 Trp Ala Ala Tyr Leu Ala Gly Gly Asp Thr Ile Tyr Leu Ala Asn Tyr
192 305 310 315 320
193 Thr Leu Pro Asp Ser Pro Phe Leu Lys Val Phe Lys Pro Glu Ala Ala
194 325 330 335
195 Phe Leu Pro Glu Trp Val Gly Ile Pro Ala Asp Leu Ser Pro Leu Leu
196 340 345 350
197 Lys Ala Leu Thr Pro Ala Cys Pro Arg Ser His Phe His Leu Lys Ala
198 355 360 365

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199      Lys Gly Val Thr Cys Tyr Val Ala Gly Arg Ala Phe
200          370                      375                      380
202 <210> SEQ ID NO: 9
203 <211> LENGTH: 1068
204 <212> TYPE: DNA
205 <213> ORGANISM: Rattus norvegicus
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (1)..(1062)
209 <400> SEQUENCE: 9
210      ctc cag cag cga ata gtg aag ctc caa ccc ctg tca gag aag gaa tta      48
211      Leu Gln Gln Arg Ile Val Lys Leu Gln Pro Leu Ser Glu Lys Glu Leu
212          1                      5                      10                      15
213      ccg atg acg act caa atg tcc tcg gga aac aca gaa agc cca gag atg      96
214      Pro Met Thr Thr Gln Met Ser Ser Gly Asn Thr Glu Ser Pro Glu Met
215          20                      25                      30
216      cga cgg gac agc gag cag cat ggg aat gga gag ctg cgg ggc atg ttc      144
217      Arg Arg Asp Ser Glu Gln His Gly Asn Gly Glu Leu Arg Gly Met Phe
218          35                      40                      45
219      acg atc aat tcc att ggc cgg ctg ggg aac cag atg ggc gaa tac gcc      192
220      Thr Ile Asn Ser Ile Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala
221          50                      55                      60
222      aca ctc ttt gca ctg gcc agg atg aac gga cgg ctt gcg ttc atc ccc      240
223      Thr Leu Phe Ala Leu Ala Arg Met Asn Gly Arg Leu Ala Phe Ile Pro
224          65                      70                      75                      80
225      gca tcc atg cac aac gct cta gcg ccc atc ttc agg atc agc ctc ccg      288
226      Ala Ser Met His Asn Ala Leu Ala Pro Ile Phe Arg Ile Ser Leu Pro
227          85                      90                      95
228      gtg tta cac agc gac acg gcc aaa aag atc cca tgg cag aat tac cat      336
229      Val Leu His Ser Asp Thr Ala Lys Lys Ile Pro Trp Gln Asn Tyr His
230          100                     105                     110
231      ctc aac gac tgg atg gag gag cgt tac cgc cac att ccg gga cac ttt      384
232      Leu Asn Asp Trp Met Glu Glu Arg Tyr Arg His Ile Pro Gly His Phe
233          115                     120                     125
234      gtg cgc ttc acg gga tac ccg tgc tcc tgg acc ttc tac cac cac ctg      432
235      Val Arg Phe Thr Gly Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu
236          130                     135                     140
237      cgc cca gag atc ctg aag gag ttc acc ctg cat gac cac gtg cgg gag      480
238      Arg Pro Glu Ile Leu Lys Glu Phe Thr Leu His Asp His Val Arg Glu
239          145                     150                     155                     160
240      gag gcc cag gcc ttc ctg cgt ggt ctg cgg gtg aat ggg agc cag ccg      528
241      Glu Ala Gln Ala Phe Leu Arg Gly Leu Arg Val Asn Gly Ser Gln Pro
242          165                     170                     175
243      agt act ttt gtg ggt gtc cat gtg cgc cga ggg gac tat gtg cat gtc      576
244      Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr Val His Val
245          180                     185                     190
246      atg cct aat gtg tgg aag ggc gtg gtg gct gac cgg ggt tac ctg gaa      624
247      Met Pro Asn Val Trp Lys Gly Val Val Ala Asp Arg Gly Tyr Leu Glu
248          195                     200                     205

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VERIFICATION SUMMARY

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